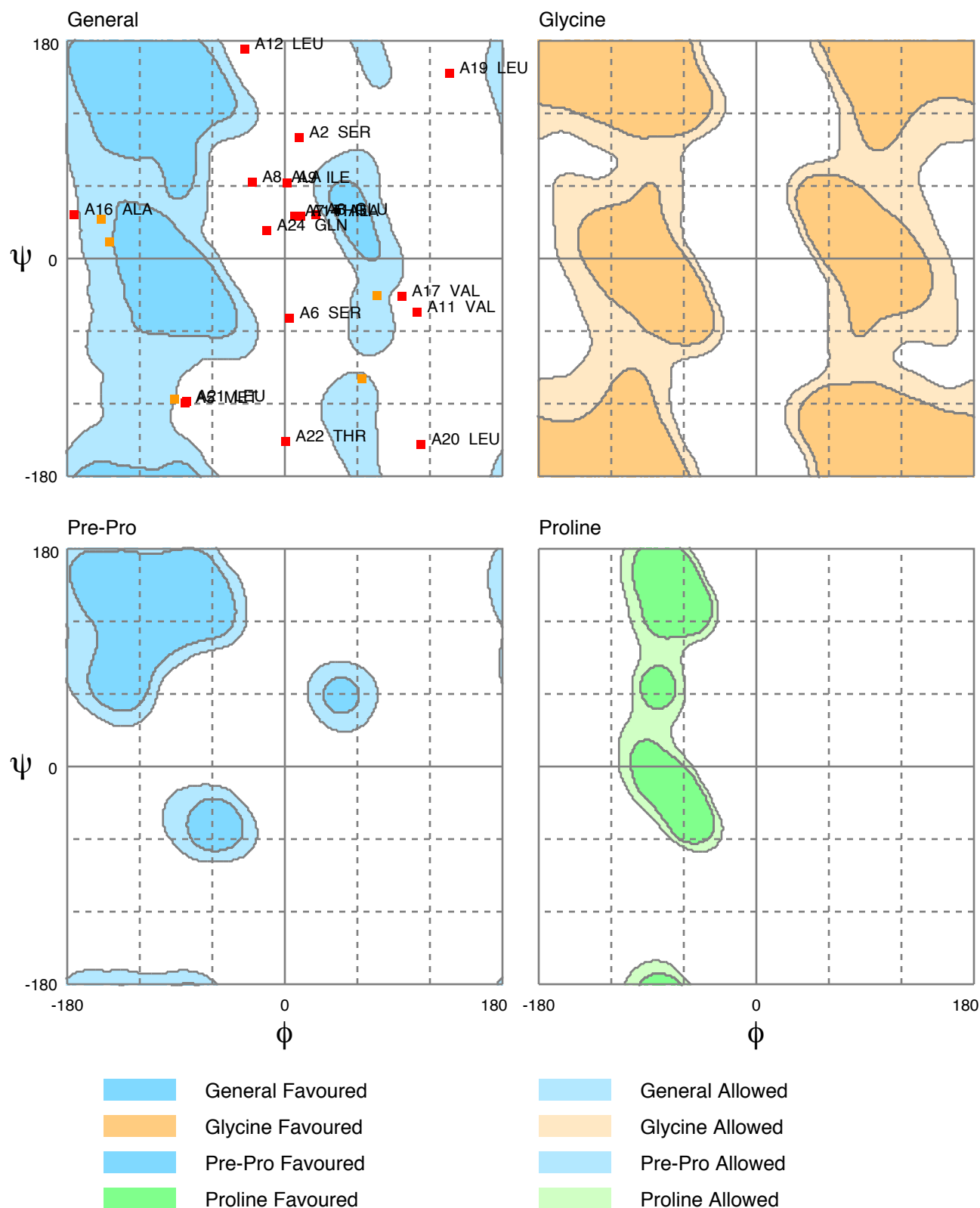


Number of residues in favoured region (~98.0% expected) : 1 (4.3%)
 Number of residues in allowed region (~2.0% expected) : 5 (21.7%)
 Number of residues in outlier region : 17 (73.9%)

RAMPAGE by Paul de Bakker and Simon Lovell available at <http://www-cryst.bioc.cam.ac.uk/rampage/>

Please cite: S.C. Lovell, I.W. Davis, W.B. Arendall III, P.I.W. de Bakker, J.M. Word, M.G. Prisant, J.S. Richardson & D.C. Richardson (2002)
 Structure validation by α geometry: ϕ/ψ and $C\beta$ deviation. *Proteins: Structure, Function & Genetics*. **50**: 437-450



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